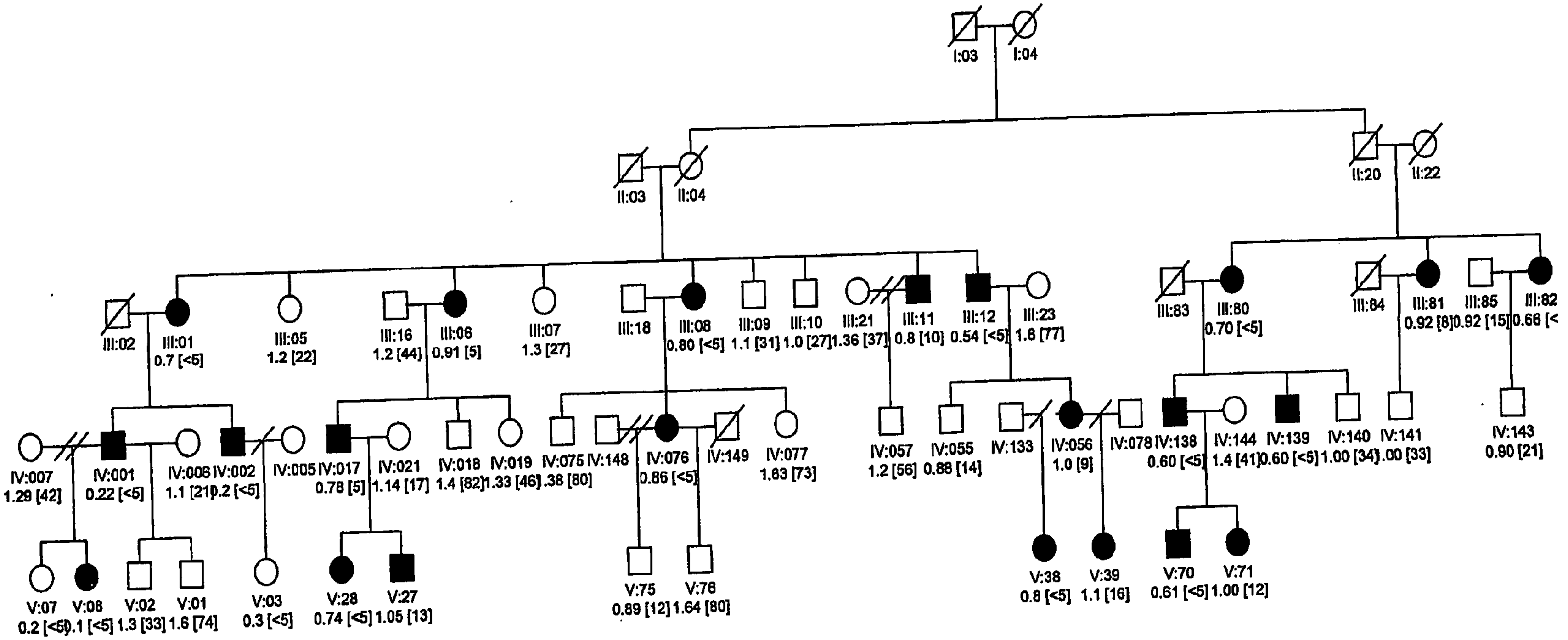
10/518868

Figure 1

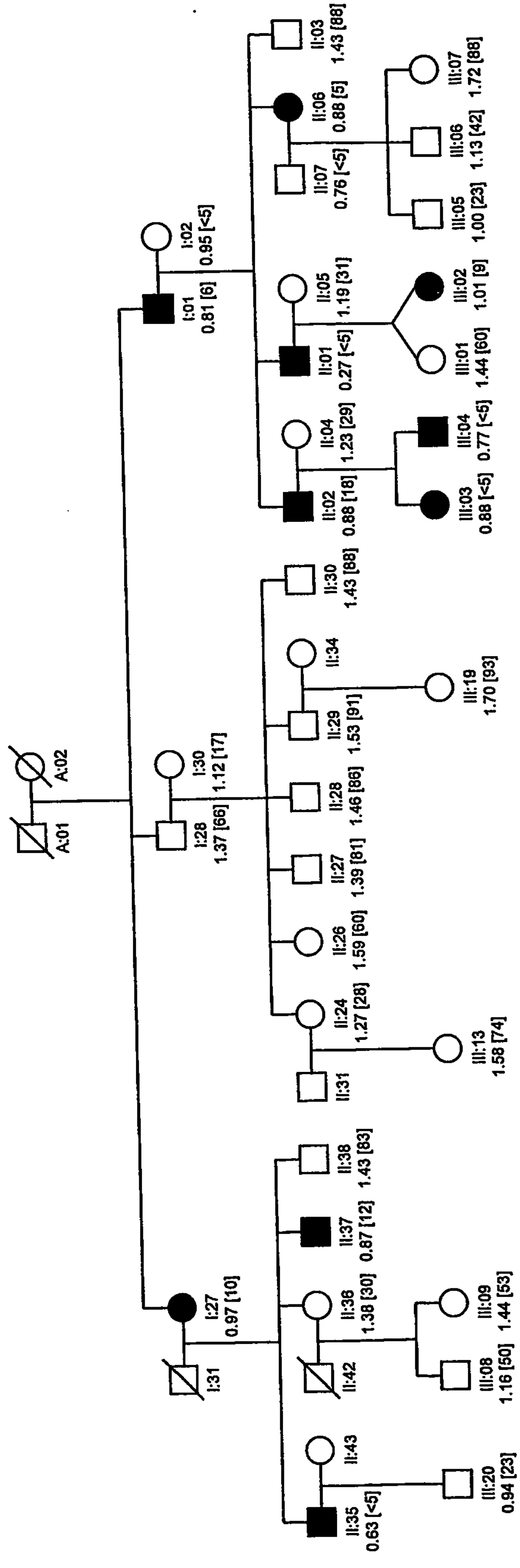
BC-11M


I:03
I:04
II:03
II:04
II:20
II:22
III:02
III:01 0.7 [<5]
III:05 1.2 [22]
III:16 1.2 [44]
III:06 0.91 [5]
III:07 1.3 [27]
III:18
III:08 0.80 [<5]
III:09 1.1 [31]
III:10 1.0 [27]
III:21 1.36 [37]
III:11 0.8 [10]
III:12 0.54 [<5]
III:23 1.8 [77]
III:83
III:80 0.70 [<5]
III:84
III:81 0.92 [8]
III:85 0.92 [15]
III:82 0.66 [<
IV:007 1.29 [42]
IV:001 0.22 [<5]
IV:008 1.1 [21]
IV:002 0.2 [<5]
IV:005
IV:017 0.78 [5]
IV:021 1.14 [17]
IV:018 1.4 [82]
IV:019 1.33 [46]
IV:075 1.38 [80]
IV:148
IV:076 0.86 [<5]
IV:149
IV:077 1.63 [73]
IV:057 1.2 [56]
IV:055 0.88 [14]
IV:133
IV:056 1.0 [9]
IV:078
IV:138 0.60 [<5]
IV:144 1.4 [41]
IV:139 0.60 [<5]
IV:140 1.00 [34]
IV:141 1.00 [33]
IV:143 0.90 [21]
V:07 0.2 [<5]
V:08 0.1 [<5]
V:02 1.3 [33]
V:01 1.6 [74]
V:03 0.3 [<5]
V:28 0.74 [<5]
V:27 1.05 [13]
V:75 0.89 [12]
V:76 1.64 [80]
V:38 0.8 [<5]
V:39 1.1 [16]
V:70 0.61 [<5]
V:71 1.00 [12]

10/518868

Figure 2

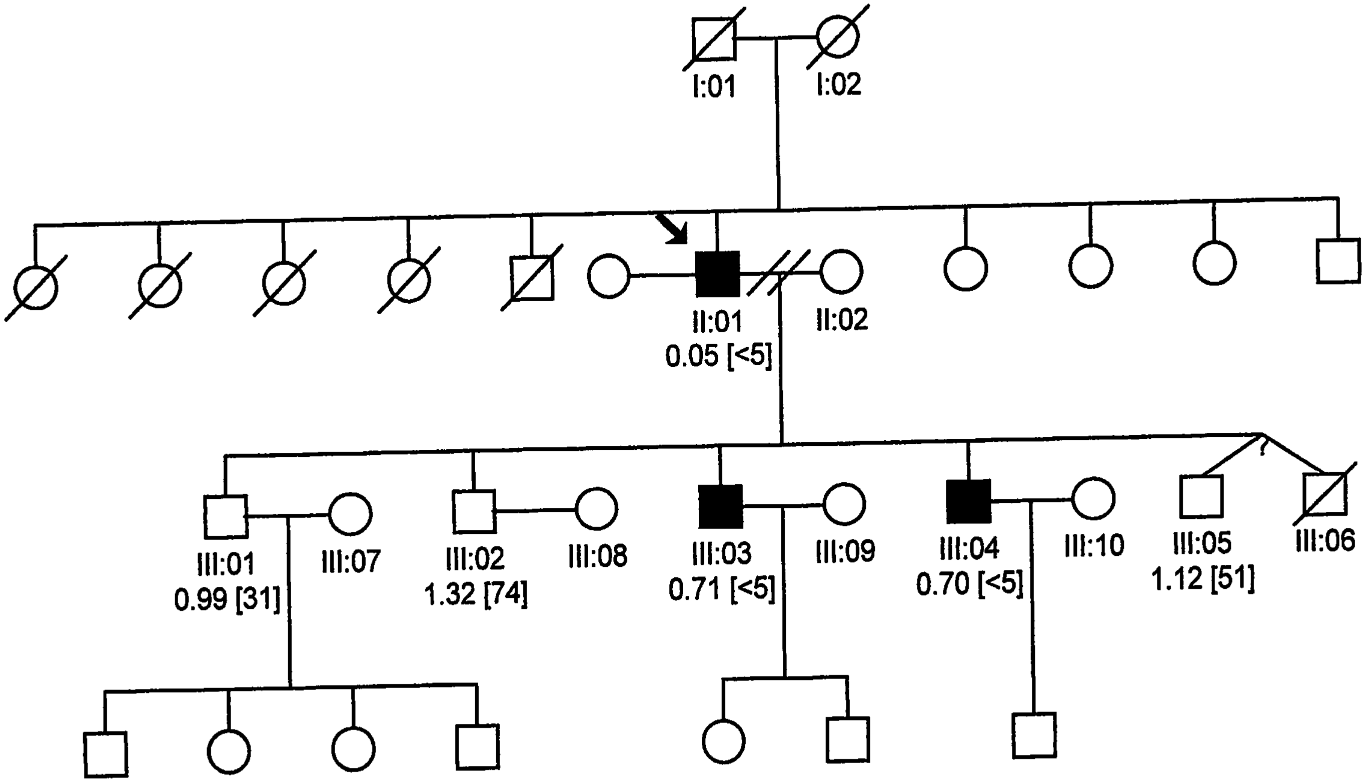
NL-003


A:01
A:02
I:01
0.81 [6]
I:02
0.95 [<5]
II:02
0.88 [18]
II:04
1.23 [29]
III:03
0.88 [<5]
III:04
0.77 [<5]
II:01
0.27 [<5]
II:05
1.19 [31]
III:01
1.44 [60]
III:02
1.01 [9]
II:07
0.76 [<5]
II:06
0.88 [5]
III:05
1.00 [23]
III:06
1.13 [42]
III:07
1.72 [88]
II:03
1.43 [88]
I:28
1.37 [66]
I:30
1.12 [17]
II:31
II:24
1.27 [28]
III:13
1.58 [74]
II:26
1.59 [60]
II:27
1.39 [81]
II:28
1.46 [86]
II:29
1.53 [91]
II:34
III:19
1.70 [93]
II:30
1.43 [88]
I:31
I:27
0.97 [10]
II:35
0.63 [<5]
II:43
III:20
0.94 [23]
II:42
II:36
1.38 [30]
III:08
1.16 [50]
III:09
1.44 [53]
II:37
0.87 [12]
II:38
1.43 [83]

10/518868

Figure 3

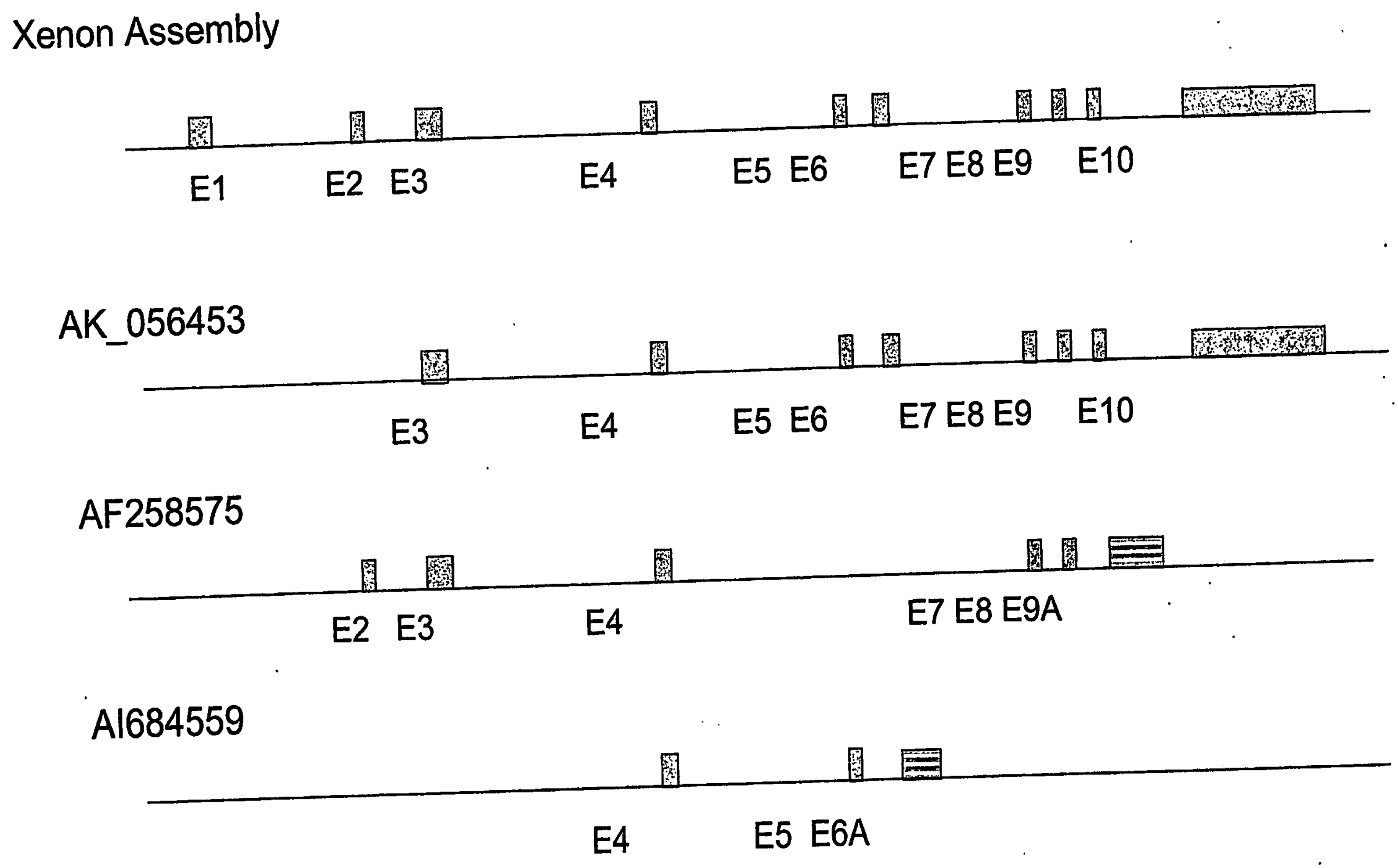
NL-120


I:01
I:02
II:01
0.05 [<5]
II:02
III:01
0.99 [31]
III:07
III:02
1.32 [74]
III:08
III:03
0.71 [<5]
III:09
III:04
0.70 [<5]
III:10
III:05
1.12 [51]
III:06

10/518868

Fig. 4

G95 – Possible Transcripts Based on Bioinformatics


Xenon Assembly
E1
E2
E3
E4
E5
E6
E7
E8
E9
E10
AK_056453
E3
E4
E5
E6
E7
E8
E9
E10
AF258575
E2
E3
E4
E7
E8
E9A
AI684559
E4
E5
E6A

10/518868

Figure 5A

```
aaggcgcgcggatgggccggcacgcaggcgcactagctcgccacggccccggaagcgcag
gagaggccgccgggtggggctaggcgctgcgacagccggcgtgaggaagctcagtgggct
acgaacgtctggcacacatgcaaccgccccctcgggctgcctccgcctgccggctacttc
tttctcccgccttccgctc

 E1: ATGTCCTTCCGGGGCCACGCAGAAAGTGCCGCCGCTTTGGCCACTCAGAGC
 +2:   C  P  S  G  A  T  Q  K  V  P  P  L  W  P  L  R  A
 E1: CCCCGGGCCGCGGTCGTCGTACGCCTGAAGGCGGGTCGTGCCGGCGGCCGC
 +2:   P  G  P  R  S  S  Y  A  *  R  R  V  V  P  A  A  A
 E1: TCTAGTCTCCGCCTCCGCTCAGGCCGGTCCTCCGGGGCTTCTCAATGGTTT
 +2:   L  V  S  A  S  A  Q  A  G  P  P  G  L  L  N  G  F
 E1: CCCGGTGGCCTCTCAATGGTTTTCCCGGCGGCCCTTGCGCCGACGCCAGGA
 +2:   P  V  A  S  Q  W  F  S  R  R  P  L  R  R  R  Q  E
 E1: GACTTCCGGAGCTTGGTGACGTCACGAGCGAGCTTTTCTACCCAAATACGC
 +2:   T  S  G  A  W  *  R  H  E  R  A  F  L  P  K  Y  A
 E1: GGCGGGGGAATAGGCTCGAGGGCGGTGAGCAGTGACAATTGCTAGGCGGAG
 +2:   A  G  E  *  A  R  G  R  *  A  V  T  I  A  R  R  R
 E1: ACAGTGCAGGGAAGAGAGACCTTAGAAAGGATCAGGACTGGCGG
 +2:   Q  C  R  E  E  R  P  *  K  G  S  G  L  A   G

                  gtatgt...cttatttatattctag

 E2: GAGGTATTTAACTGAAAGGAATATCTGCTTCACTGTTGCAACCAAACCAGA
 +3:    G  I  *  L  K  G  I  S  A  S  L  L  Q  P  N  Q  M
 E2: TGCCTTCTTCCACTTCACCAGACCAAGGAGATGACCTGGAGAACTGCATTT
 +3:    P  S  S  T  S  P  D  Q  G  D  D  L  E  N  C  I  L
 E2: TAAGATTTTCTGACCTGGATTTAAAAGATATGAGTCTTATTAATCCCAGCA
 +3:    R  F  S  D  L  D  L  K  D  M  S  L  I  N  P  S  S
 E2: GCAGTCTTAAAGCAGAATTAGATGGCAGTACAAAAAAGAAATACTCGTTTG0
 +3:    S  L  K  A  E  L  D  G  S  T  K  K  K  Y  S  F  A
 E2: CAAAGAAAAAG
 +3:    K  K  K

                  gtagaa...
```

10/518868

Figure 5B

```
                ...tgaaatctaattgcag

E3:  GCCTTTGCCCTTTTTGTCAAAACCAAAGAAGTTCCAACAAAAAGGAGTTTT
+1:  A  F  A  L  F  V  K  T  K  E  V  P  T  K  R  S  F
E3:  GAATGTAAAGAAAAATTGTGGAAATGCTGTCGGCAGCTATTCACAGACCAA
+1:  E  C  K  E  K  L  W  K  C  C  R  Q  L  F  T  D  Q
E3:  ACCAGCATCCATAGACATGTGGCAACACAACATGCTGATGAAATTTATCAC
+1:  T  S  I  H  R  H  V  A  T  Q  H  A  D  E  I  Y  H
E3:  CAGACAGCTTCTATTTTAAAGCAACTGGCTGTGACATTGAGCACCTCAAAG
+1:  Q  T  A  S  I  L  K  Q  L  A  V  T  L  S  T  S  K
E3:  AGTCTTTCGTCTGCAGATGAAAAGAACCCTTTAAAAGAGTGCCTTCCACAT
+1:  S  L  S  S  A  D  E  K  N  P  L  K  E  C  L  P  H
E3:  AGCCATGACGTGTCTGCTTGGCTCCCTGATATAAGCTGCTTTAACCCTGAT
+1:  S  H  D  V  S  A  W  L  P  D  I  S  C  F  N  P  D
E3:  GAGCTGATAAG
+1:  E  L  I   S


            gtaaga...gattttcattttatag


E4:  TGGCCAGGGCAGTGAAGAAGGGGAGGTGCTCCTTTATTACTGCTACCATGA
+2:   G  Q  G  S  E  E  G  E  V  L  L  Y  Y  C  Y  H  D
E4:  CCTGGAGGATCCCCAATGGATCTGTGCCTGGCAGACAGCTCTGTGTCAGCA
+2:   L  E  D  P  Q  W  I  C  A  W  Q  T  A  L  C  Q  H
E4:  CCTGCACCTCACAGGCAAG
+2:   L  H  L  T  G  K

                    gtaaca...ccgtcttgtgtctcag

E5:  ATTCGAATTGCTGCAGAAGGAATCAATGGGACAGTTGGTGGAAGCAAATTG
+1:  I  R  I  A  A  E  G  I  N  G  T  V  G  G  S  K  L
E5:  GCTACCAGACTTTATGTGGAAGTCATGCTTTCCTTCCCATTGTTTAAGGAT
+1:  A  T  R  L  Y  V  E  V  M  L  S  F  P  L  F  K  D
E5:  GACCTGTGTAAAGATGATTTTAAG
+1:  D  L  C  K  D  D  F  K

                    gtaaga...
```

10/518868

Figure 5C

```
               ...gtttctcattggctag

E6: ACCAGCAAAGGAGGAGCTCACTGTTTTCCAGAATTGCGTGTTGGTGTATTT
+1: T  S  K  G  G  A  H  C  F  P  E  L  R  V  G  V  F
E6: GAAGAAATCGTGCCCATGGGGATCAGCCCCAAAAAGATCTCCTACAAGAAG
+1: E  E  I  V  P  M  G  I  S  P  K  K  I  S  Y  K  K
E6: CCTG
+1: P  G

        gtatgc...tttggtttggttttag

E7: GAATCCATTTATCCCCAGGTGAATTTCATAAAGAAGTAGAAAAGTTTTTAT
+3:   I  H  L  S  P  G  E  F  H  K  E  V  E  K  F  L  S
E7: CTCAGGCAAATCAAGAACAAAGTGATACTATCCTTCTTGATTGCAGAAACT
+3:   Q  A  N  Q  E  Q  S  D  T  I  L  L  D  C  R  N  F
E7: TCTATGAAAGCAAAATA
+3:   Y  E  S  K  I

        gtaagt...tgctcctatgttacag

E8: GGACGATTCCAAGGCTGCTTAGCCCCAGACATCAGGAAATTCAGTTACTTC
+1: G  R  F  Q  G  C  L  A  P  D  I  R  K  F  S  Y  F
E8: CCTAGCTACGTTGACAAAAATCTAGAACTTTTCAGAGAGAAGAGAGTGCTG
+1: P  S  Y  V  D  K  N  L  E  L  F  R  E  K  R  V  L
E8: ATGTACTGTACCGGGGGCATCCGCTGTGAGCGGGGTTCAGCCTACCTCAAA
+1: M  Y  C  T  G  G  I  R  C  E  R  G  S  A  Y  L  K
E8: GCCAAG
+1: A  K

        gtgagc...gtttttccacacctag

E9: GGAGTGTGCAAGGAGGTGTTCCAGCTCAAGGGTGGCATCCACAAGTACCTG
+1: G  V  C  K  E  V  F  Q  L  K  G  G  I  H  K  Y  L
E9: GAAGAGTTTCCTGATGGCTTTTACAAAGGGAAGTTGTTTGTTTTTGATGAA
+1: E  E  F  P  D  G  F  Y  K  G  K  L  F  V  F  D  E
E9: CGCTATGCTCTGTCCTACAACAGTGATGTGGTGTCAG
+1: R  Y  A  L  S  Y  N  S  D  V  V  S   E

        gtaggt...
```

10/518868

Figure 5D

```
                  ...tttccttcctccccag

E10: AGTGTTCATACTGTGGAGCCCGCTGGGACCAGTATAAACTCTGCTCTACTC
 +3:  C  S  Y  C  G  A  R  W  D  Q  Y  K  L  C  S  T  P
E10: CCCAGTGCCGCCAGCTCGTTTTGACCTGCCCTGCCTGTCAAGGACAAGGAT
 +3:  Q  C  R  Q  L  V  L  T  C  P  A  C  Q  G  Q  G  F
E10: TCACAGCCTGTTGTGTCACATGTCAAGACAAGGGGAGCAGGAAAGTTTCAG
 +3:  T  A  C  C  V  T  C  Q  D  K  G  S  R  K  V  S  G
E10: GCCCTATGCAAGACAGCTTTAAAGAGGAATGCGAGTGCACAGCCCGACGGC
 +3:  P  M  Q  D  S  F  K  E  E  C  E  C  T  A  R  R  P
E10: CACGCATACCTAGGGAACTCTTGCAGCATGTGCGACAGCCTGTGAGCCCAG
 +3:  R  I  P  R  E  L  L  Q  H  V  R  Q  P  V  S  P  E
E10: AGCCAGGGCCTGATGCTGATGAGGATGGGCCAGTGCTTATGTGAGCAGCAC
 +3:  P  G  P  D  A  D  E  D  G  P  V  L  M  *  A  A  P
E10: CTTTGGCATTTTCCCAGGCCCTCGGTAAAAGTAGGTTTGGGGTGACTATAC
 +3:  L  A  F  S  Q  A  L  G  K  S  R  F  G  V  T  I  Q
E10: AGAGAAAGCATGGCAAGACTGCAGAAACAGAGAAATCGGGAACTTCAGTTC
 +3:  R  K  H  G  K  T  A  E  T  E  K  S  G  T  S  V  L
E10: TGGCCGCTGCCACCGTGGCAGCCGTCTACACTTCACAGCGGGAGGGGAGGA
 +3:  A  A  A  T  V  A  A  V  Y  T  S  Q  R  E  G  R  S
E10: GTCACGTTGTCTACCACTTACCTGAGACATTCTGATTTGGATGATGCTAGA
 +3:  H  V  V  Y  H  L  P  E  T  F  *  F  G  *  C  *  S
E10: GCACAGAAAATAGGTGAGCTGCATGGGATCCCAAAGCTGCTGAGGGATAGA
 +3:  T  E  N  R  *  A  A  W  D  P  K  A  A  E  G  *  S
E10: GCCTGAGCCTGGTGGCCACAGCATATGCCCTTTCTGTTCCATGCAGCTGGG
 +3:  L  S  L  V  A  T  A  Y  A  L  S  V  P  C  S  W  G
E10: GCTGTTAGTAGTCATTGCCCTTGTCAGCAGACCTTCTACCCTGGTGGCAAA
 +3:  C  *  *  S  L  P  L  S  A  D  L  L  P  W  W  Q  T
E10: CACATGAAAGCTGTGGCCCTGGGAGTGGCCTCCTAAAACAAGCCACTTAGG
 +3:  H  E  S  C  G  P  G  S  G  L  L  K  Q  A  T  *  V
E10: TCATCTGCCATCTACCCTTAACCTCTGTCTCTCGCCTGAGGGGAATCTGCA
 +3:  I  C  H  L  P  L  T  S  V  S  R  L  R  G  I  C  K
E10: AGCTGTGCATTGGGCTTACCTCCTGCTTTTGTAGAAATAACCATCCTTTGG
 +3:  L  C  I  G  L  T  S  C  F  C  R  N  N  H  P  L  V
E10: TATACATGGAGGATAGTTCCAGAACGCCTGAGTATACAAAAACCCAATGCA
 +3:  Y  M  E  D  S  S  R  T  P  E  Y  T  K  T  Q  C  I
E10: TACTCAAGTCCCACAGTGGGCCCTACAGAACCCACGTATGTGATAAATCAG
 +3:  L  K  S  H  S  G  P  Y  R  T  H  V  C  D  K  S  A
E10: CCCTCCATGTACGCAGGTTTCGCCCCCTGCCAATACTGTATTTTCAACCTG
 +3:  L  H  V  R  R  F  R  P  L  P  I  L  Y  F  Q  P  V
E10: TATGGTTGAAAAAAATCCATATATAAGTGCAGCCATGCAGTTCAAACCCAT
 +3:  W  L  K  K  I  H  I  *  V  Q  P  C  S  S  N  P  Y
E10: ATTGTTCAAGGGTCAACTGTATAGTTTATTGAACAGCCACACCCATTCCTT
 +3:  C  S  R  V  N  C  I  V  Y  *  T  A  T  P  I  P  L
E10: TACACATGATCTATGGCAGAGTTGAATAGTTGCAACAGACACTATGTGGCC
 +3:  H  M  I  Y  G  R  V  E  *  L  Q  Q  T  L  C  G  L
```

10/518868

Figure 5E

```
E10: TGCAAAATCGGAAATTTTTACTGTCTGGCCTTTTACAGAAAAGTTTGCCAG
 +3:    Q  N  R  K  F  L  L  S  G  L  L  Q  K  S  L  P  A
E10: CCCCTGATCTAGACCAGCAGCTCATCTGATAGAGGCAGAGGTGGCCTTAAA
 +3:    P  D  L  D  Q  Q  L  I  *  *  R  Q  R  W  P  *  R
E10: GATGTGGCCTTCTTCATTTTCTGTTGGTTTGGTTTCGTTTCTATGAGAGAT
 +3:    C  G  L  L  H  F  L  L  V  W  F  R  F  Y  E  R  F
E10: TTCCTCTGATAGCTCTGCTTTCCCCAGCACTTACTCTCTGAGCTTTTAAAT
 +3:    P  L  I  A  L  L  S  P  A  L  T  L  *  A  F  K  C
E10: GTTCTCTCTGGGAGCTTCATATAAGCTCGGTGACATTTGAGCCACAGTTTT
 +3:    S  L  W  E  L  H  I  S  S  V  T  F  E  P  Q  F  L
E10: TAGATCAGCACCTGGAATACATGACACATTCTTACTGAGGTCATCCAGCAC
 +3:    D  Q  H  L  E  Y  M  T  H  S  Y  *  G  H  P  A  L
E10: TGCCATGGTGGCTGCCCAGTCTTCTGGCCAGTGTGCCAGGCACATGTCCCT
 +3:    P  W  W  L  P  S  L  L  A  S  V  P  G  T  C  P  C
E10: GTCACACAGGTTCCAAGAAACACATACGCAGCCATGCATAGACCAACAGAT
 +3:    H  T  G  S  K  K  H  I  R  S  H  A  *  T  N  R  F
E10: TTAATATTATATTGCAGTTTTCAGCGATGCAGAATGCAGCTGCAATTGTGT
 +3:    N  I  I  L  Q  F  S  A  M  Q  N  A  A  A  I  V  F
E10: TTTAAGGAGAAGCCAAATGGGGATGGTTGTCCCTGCAACATGGTGCCACTC
 +3:    *  G  E  A  K  W  G  W  L  S  L  Q  H  G  A  T  P
E10: CTGGGCCATGTGCAGCCTCAGTGGACACTCTTCCATAGCGCTGAGGCCCTG
 +3:    G  P  C  A  A  S  V  D  T  L  P  *  R  *  G  P  G
E10: GCCCCGCCTCCAGTTACCCTGTACTGCCCACTGCCTTACAGTTCAGTGCGC
 +3:    P  A  S  S  Y  P  V  L  P  T  A  L  Q  F  S  A  Q
E10: AGGCCTTCACCTTTTCATCACCAGCCTCTCTGCTCAGTGCTCTGGAGTTCT
 +3:    A  F  T  F  S  S  P  A  S  L  L  S  A  L  E  F  L
E10: TGACCTTGTCCTTTATCATGAGATTTGCTGAAATCACTAATGAAAATAACT
 +3:    T  L  S  F  I  M  R  F  A  E  I  T  N  E  N  N  S
E10: CCCAAAAGCAACAAACAAAAATATTAGTTTAACTGGCACTGTGGTATATTA
 +3:    Q  K  Q  Q  T  K  I  L  V  *  L  A  L  W  Y  I  K
E10: AAAGGCACAAGGGCATTGTGGCTTAACACTTTTGCTGGATCCCAAGAGACG
 +3:    R  H  K  G  I  V  A  *  H  F  C  W  I  P  R  D  A
E10: CACATGATGTTAAAAAGAGATCTGGCAGCAGTACTAATACTACATTTCAGT
 +3:    H  D  V  K  K  R  S  G  S  S  T  N  T  T  F  Q  C
E10: GTAATCATCTTGGGGTGGTTTGGCCAGGATTTCCCAATTCCTTGATATCTG
 +3:    N  H  L  G  V  V  W  P  G  F  P  N  S  L  I  S  G
E10: GAGTTTCTTCACCATTGTCCGGCATCCTGCGGAGGCTTAATATACAGGCGT
 +3:    V  S  S  P  L  S  G  I  L  R  R  L  N  I  Q  A  *
E10: AAGGTCAGCAGCAATTTGTCTAATAAGTGATGAGATCAGTAGCTGAAGTCT
 +3:    G  Q  Q  Q  F  V  *  *  V  M  R  S  V  A  E  V  S
E10: CTAAGCTGGGCCATTACTAAATACCATAGCCATGTTGATCTGGAAATTTAT
 +3:    K  L  G  H  Y  *  I  P  *  P  C  *  S  G  N  L  S
E10: CCCTCTAGTGTCTTACCTCACATAAGCCATTTGCCCACTGTGCAATATAGA
 +3:    L  *  C  L  T  S  H  K  P  F  A  H  C  A  I  *  K
E10: AAGGTGTTTTCAAAAGTATTTGGCCGTAGATTTTCACATCCATCATAAGGT
 +3:    G  V  F  K  S  I  W  P  *  I  F  T  S  I  I  R  L
```

10/518868

Figure 5F

```
E10: TGGCATTCAATAAGGAAAAAGTTCTAACTCCAGTATTAAATTGTACATAAA
 +3:  A  F  N  K  E  K  V  L  T  P  V  L  N  C  T  *  I
E10: TCCCAAATGTTCTTAAAGAACACTCAGGGACATGTTTGTTGCCTGGGATTG
 +3:  P  N  V  L  K  E  H  S  G  T  C  L  L  P  G  I  G
E10: GTAATGAAAGGTTGGTTTTTGAAACTTGAAATTTCACCATTGGTTTTTTTC
 +3:  N  E  R  L  V  F  E  T  *  N  F  T  I  G  F  F  P
E10: CTATCATTTCTGCATATCCAGCAAAAGGAATCTCATGTTGACTCCTGGCAG
 +3:  I  I  S  A  Y  P  A  K  G  I  S  C  *  L  L  A  E
E10: AGTTCAGTGGCTTCAGTCTGTCTATCTGTTCTGAGGGGAAAATTGTGTTCT
 +3:  F  S  G  F  S  L  S  I  C  S  E  G  K  I  V  F  W
E10: GGATCCAGTAATCAATTTGGCAACTTTAATCGAGGTTTTCAAAATTCCAAG
 +3:  I  Q  *  S  I  W  Q  L  *  S  R  F  S  K  F  Q  G
E10: GAGGGTTAATAAAGAATGATAATCAGTTTTATTTGCTAATAGCTAAGACAA
 +3:  G  L  I  K  N  D  N  Q  F  Y  L  L  I  A  K  T  N
E10: ATTTGTAATAAAGTGTTTTATAATACTTC
 +3:  L  *  *  S  V  L  *  Y  F
```

```
        ...gtgcttttctctttag

E6a: GTTACGAGACAGTACAATAGAAGGAGTATGCTCGTCCCCATTCTTTCACTG
 +1: V  T  R  Q  Y  N  R  R  S  M  L  V  P  I  L  S  L
E6a: AGTCACCATATGATTTTGGACCAGCTAGTGCTCTAGACCTCAGTATCCCTT
 +1: S  H  H  M  I  L  D  Q  L  V  L  *  T  S  V  S  L
E6a: CTTATAAAATAAGAATGTTACAGCTCATGCAATCTGGGACTCCAAATCTTG
 +1: L  I  K  *  E  C  Y  S  S  C  N  L  G  L  Q  I  L
E6a: GACATATTAGCTCACTTGAGAGACCACCAGCCTGGTCAGCAGATCACTGTG
 +1: D  I  L  A  H  L  R  D  H  Q  P  G  Q  Q  I  T  V
E6a: TTTTTAGTAAATCTGGAATTGTAAGATTAACACTTCATACCACATGGGGGA
 +1: F  L  V  N  L  E  L  *  D  *  H  F  I  P  H  G  G
E6a: ATAAAGTTGTTGCTCTCACAGGT
 +1: I  K  L  L  L  S  Q

                 gggctg...
```

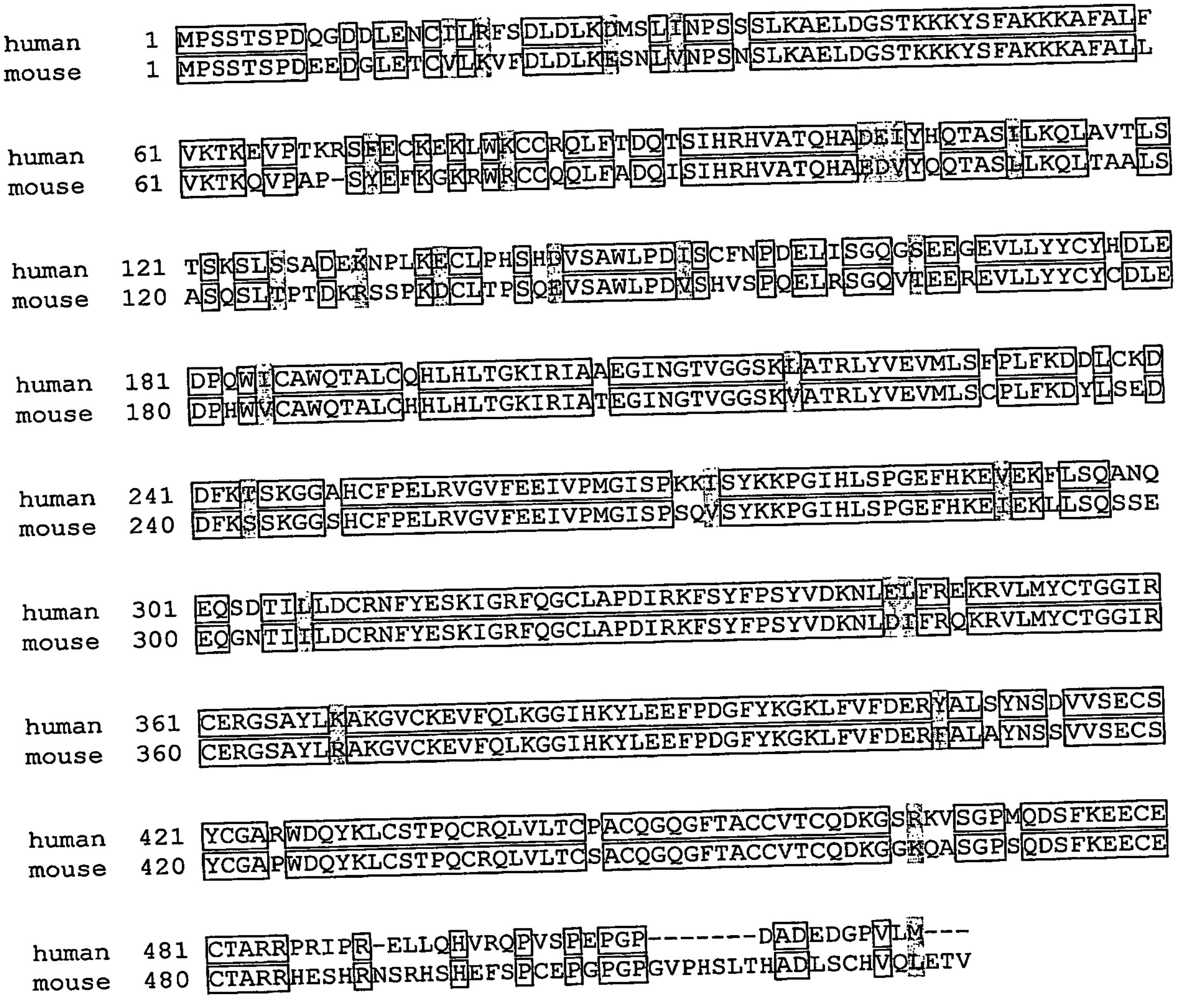
10/518848

Figure 5G

```
        ...gtttttccacacctag

E9a: GGAGTGTGCAAGGAGGTGTTCCAGCTCAAGGGTGGCATCCACAAGTACCTG
 +1: G  V  C  K  E  V  F  Q  L  K  G  G  I  H  K  Y  L
E9a: GAAGAGTTTCCTGATGGCTTTTACAAAGGGAAGTTGTTTGTTTTTGATGAA
 +1: E  E  F  P  D  G  F  Y  K  G  K  L  F  V  F  D  E
E9a: CGCTATGCTCTGTCCTACAACAGTGATGTGGTGTCAGGTAGGTCAGCACAG
 +1: R  Y  A  L  S  Y  N  S  D  V  V  S  G  R  S  A  Q
E9a: GCTCAGAGCCCAAACTGAAATGAAGCACATTGTCAGTTCACTATTCTAGAA
 +1: A  Q  S  P  N  *  N  E  A  H  C  Q  F  T  I  L  E
E9a: AAATGACACAGGGAAGACAGGCCAGTGCTCATTACTGAGCACTGAATAAGC
 +1: K  *  H  R  E  D  R  P  V  L  I  T  E  H  *  I  S
E9a: AGGGAAAATAAGTACATTGTGCCACCATTTTCCCAGCTGTGGAGCTGAGAG
 +1: R  E  N  K  Y  I  V  P  P  F  S  Q  L  W  S  *  E
E9a: AACCCTAGCCCAGGAGTCAGGAGGCCTGGGTTGGGATCCTGGCTTCACCAT
 +1: N  P  S  P  G  V  R  R  P  G  L  G  S  W  L  H  H
E9a: TGCTAGCTGGACAAGCCCATTAACATGGGGATCATCTCACCTGCCCTGCCT
 +1: C  *  L  D  K  P  I  N  M  G  I  I  S  P  A  L  P
E9a: GCCTGTCTACCTGCCAAGAGCTGTACTACTGGGCTAATTCAGGGCTCTTAA
 +1: A  C  L  P  A  K  S  C  T  T  G  L  I  Q  G  S  *
E9a: CCTGGAATTGGTACATAGATTTCAGGGATTCTGTGAATTTGGATGGAAAAA
 +1: P  G  I  G  T  *  I  S  G  I  L  *  I  W  M  E  K
E9a: TAATTGTATCTTTGTTTTCAATAACACCTCACTAAAATGAAGCATTTCCTT
 +1: *  L  Y  L  C  F  Q  *  H  L  T  K  M  K  H  F  L
E9a: TAGTTATGAATGTAGGCAACAAAGTACCAGTTGTATTAATGTACCTGTGAC
 +1: *  L  *  M  *  A  T  K  Y  Q  L  Y  *  C  T  C  D
E9a: TTTGTCTTCAGTAGGATTCACAATACTTTCATATCATGTTCTAGTTGCCTC
 +1: F  V  F  S  R  I  H  N  T  F  I  S  C  S  S  C  L
E9a: AGATATCTCAAAATAGTATTTATACTCATCACTGCTTCAAAATGAAAATAG
 +1: R  Y  L  K  I  V  F  I  L  I  T  A  S  K  *  K  *
E9a: TTATTAGGCCCACCACTAAGAGTTGATATATAATGTGTTAATAAATGGCAC
 +1: L  L  G  P  P  L  R  V  D  I  *  C  V  N  K  W  H
E9a: GTCTTATTATATATTACAGATTTTGAAAAAGA
 +1: V  L  L  Y  I  T  D  F  E  K

                    ...ctttga
```

10/518868

Figure 6



```
human    1  MPSSTSPDQGDDLENCILRFSDLDLKDMSLINPSSSLKAELDGSTKKKYSFAKKKAFALF
mouse    1  MPSSTSPDEEDGLETCVLKVFDLDLKESNLVNPSNSLKAELDGSTKKKYSFAKKKAFALL

human   61  VKTKEVPTKRSFECKEKLWKCCRQLFTDQTSIHRHVATQHADEIYHQTASILKQLAVTLS
mouse   61  VKTKQVPAP-SYEFKGKRWRCCQQLFADQISIHRHVATQHAEDVYQQTASLLKQLTAALS

human  121  TSKSLSSADEKNPLKECLPHSHDVSAWLPDISCFNPDELISGQGSEEGEVLLYYCYHDLE
mouse  120  ASQSLTPTDKRSSPKDCLTPSQEVSAWLPDVSHVSPQELRSGQVTEEREVLLYYCYCDLE

human  181  DPQWICAWQTALCQHLHLTGKIRIAAEGINGTVGGSKLATRLYVEVMLSFPLFKDDLCKD
mouse  180  DPHWVCAWQTALCHHLHLTGKIRIATEGINGTVGGSKVATRLYVEVMLSCPLFKDYLSED

human  241  DFKTSKGGAHCFPELRVGVFEEIVPMGISPKKISYKKPGIHLSPGEFHKEVEKFLSQANQ
mouse  240  DFKSSKGGSHCFPELRVGVFEEIVPMGISPSQVSYKKPGIHLSPGEFHKEIEKLLSQSSE

human  301  EQSDTILLDCRNFYESKIGRFQGCLAPDIRKFSYFPSYVDKNLELFREKRVLMYCTGGIR
mouse  300  EQGNTIILDCRNFYESKIGRFQGCLAPDIRKFSYFPSYVDKNLDIFRQKRVLMYCTGGIR

human  361  CERGSAYLKAKGVCKEVFQLKGGIHKYLEEFPDGFYKGKLFVFDERYALSYNSDVVSECS
mouse  360  CERGSAYLRAKGVCKEVFQLKGGIHKYLEEFPDGFYKGKLFVFDERFALAYNSSVVSECS

human  421  YCGARWDQYKLCSTPQCRQLVLTCPACQGQGFTACCVTCQDKGSRKVSGPMQDSFKEECE
mouse  420  YCGAPWDQYKLCSTPQCRQLVLTCSACQGQGFTACCVTCQDKGGKQASGPSQDSFKEECE

human  481  CTARRPRIPR-ELLQHVRQPVSPEPGP-------DADEDGPVLM---
mouse  480  CTARRHESHRNSRHSHEFSPCEPGPGPGVPHSLTHADLSCHVQLETV
```

Legend:
Identical amino acids: SL
SL

Similar amino acids: SK
TR

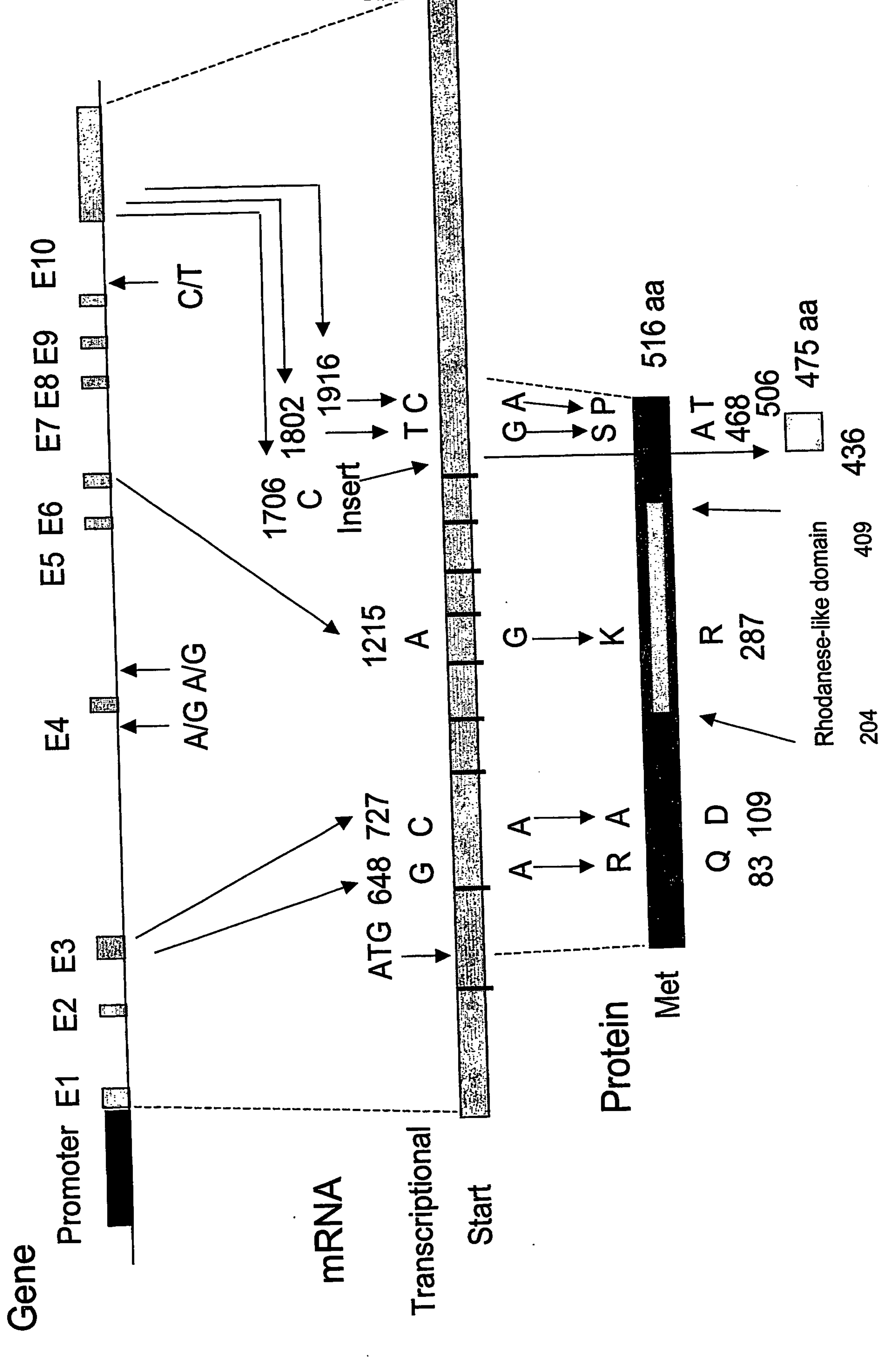
10/518868

Figure 7

```
P1G95-1   LKGISASLLQPNQMPSSTSPDQGDDLENCILRFSDLDLKDMSLINPSSSLKAELDGSTKK
P1G95-2   LKGISASLLQPNQMPSSTSPDQGDDLENCILRFSDLDLKDMSLINPSSSLKAELDGSTKK
P1G95-n   LKGISASLLQPNQMPSSTSPDQGDDLENCILRFSDLDLKDMSLINPSSSLKAELDGSTKK
          ************************************************************

P1G95-1   KYSFAKKKAFALFVKTKEVPTKRSFECKEKLWKCCRQLFTDQTSIHRHVATQHADEIYHQ
P1G95-2   KYSFAKKKAFALFVKTKEVPTKRSFECKEKLWKCCRQLFTDQTSIHRHVATQHADEIYHQ
P1G95-n   KYSFAKKKAFALFVKTKEVPTKRSFECKEKLWKCCRQLFTDQTSIHRHVATQHADEIYHQ
          ************************************************************

P1G95-1   TASILKQLAVTLSTSKSLSSADEKNPLKECLPHSHDVSAWLPDISCFNPDELISGQGSEE
P1G95-2   TASILKQLAVTLSTSKSLSSADEKNPLKECLPHSHDVSAWLPDISCFNPDELISGQGSEE
P1G95-n   TASILKQLAVTLSTSKSLSSADEKNPLKECLPHSHDVSAWLPDISCFNPDELISGQGSEE
          ************************************************************

P1G95-1   GEVLLYYCYHDLEDPQWICAWQTALCQHLHLTGKIRIAAEGINGTVGGSKLATRLYVEVM
P1G95-2   GEVLLYYCYHDLEDPQWICAWQTALCQHLHLTGKIRIAAEGINGTVGGSKLATRLYVEVM
P1G95-n   GEVLLYYCYHDLEDPQWICAWQTALCQHLHLTGKIRIAAEGINGTVGGSKLATRLYVEVM
          ************************************************************

P1G95-1   LSFPLFKDDLCKDDFKTSKGGAHCFPELRVGVFEEIVPMGISPKKISYKKPGIHLSPGEF
P1G95-2   LSFPLFKDDLCKDDFKTSKGGAHCFPELRVGVFEEIVPMGISPKKISYKKPGIHLSPGEF
P1G95-n   LSFPLFKDDLCKDDFKTSKGGAHCFPELRVGVFEEIVPMGISPKKISYKKPGIHLSPGEF
          ************************************************************

P1G95-1   HKEVEKFLSQANQEQSDTILLDCRNFYESKIGRFQGCLAPDIRKFSYFPSYVDKNLELFR
P1G95-2   HKEVEKFLSQANQEQSDTILLDCRNFYESKIGRFQGCLAPDIRKFSYFPSYVDKNLELFR
P1G95-n   HKEVEKFLSQANQEQSDTILLDCRNFYESKIGRFQGCLAPDIRKFSYFPSYVDKNLELFR
          ************************************************************

P1G95-1   EKRVLMYCTGGIRCERGSAYLKAKGVCKEVFQLKGGIHKYLEEFPDGFYKGKLFVFDERY
P1G95-2   EKRVLMYCTGGIRCERGSAYLKAKGVCKEVFQLKGGIHKYLEEFPDGFYKGKLFVFDERY
P1G95-n   EKRVLMYCTGGIRCERGSAYLKAKGVCKEVFQLKGGIHKYLEEFPDGFYKGKLFVFDERY
          ************************************************************

P1G95-1   ALSYNSDVVSECSYCGARWDQYKLCSTPQCRQLVLTCPACQGQGFTACCVTCQDKGSRKV
P1G95-2   ALSYNSDVVSECSYCGARWDQYKLCSTPPVPPARFDLPCLSRTRIHSLLCHMSRQGEQES
P1G95-n   ALSYNSDVVSECSYCGARWDQYKLCSTPQCRQLVLTCPACQGQGFTACCVTCQDKGSRKV
          ****************************      :  *. .   : :     . :*.::

P1G95-1   AGPMQDSFKEECECTARRPRIPRELLQHVRQPVSPEPGPDADEDGPVLM
P1G95-2   FRPYARQL-----------------------------------------
P1G95-n   SGPMQDSFKEECECTARRPRIPRELLQHVRQPVSPEPGPDADEDGPVLM
            *   .:   . .:   .  .         ..:. ... *   ...
```

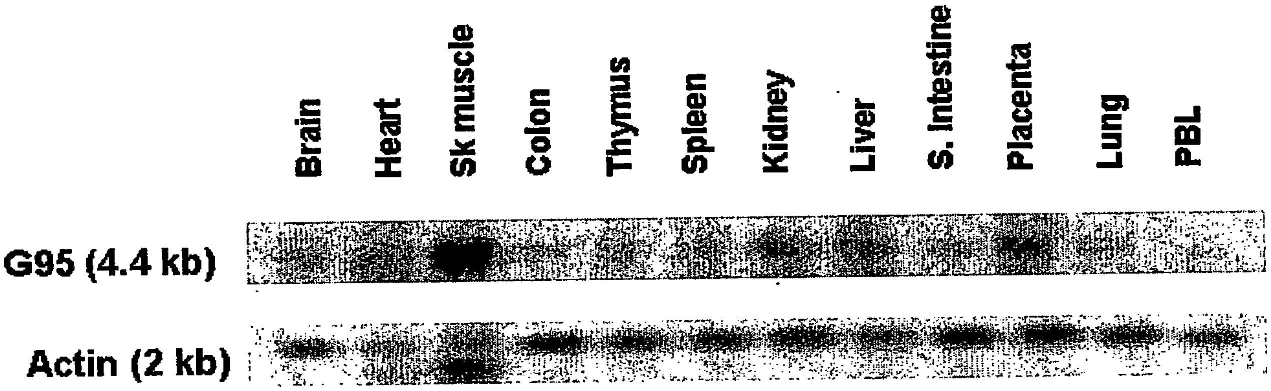
10/518868

Figure 8


Gene
Promoter
E1
E2
E3
E4
E5
E6
E7
E8
E9
E10
A/G
A/G
C/T
mRNA
Transcriptional Start
ATG
648
G
727
C
1215
A
1706
C
Insert
1802
T
1916
C
A
A
G
G
A
R
A
K
S
P
Protein
Met
Q
83
D
109
R
287
A
T
468
506
436
516 aa
475 aa
Rhodanese-like domain
204
409

10/518868

FIGURE 9


Brain
Heart
Sk muscle
Colon
Thymus
Spleen
Kidney
Liver
S. Intestine
Placenta
Lung
PBL
G95 (4.4 kb)
Actin (2 kb)